

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:	Group Art Unit: Not yet assigned
Baker et al.	Examiner: Not yet assigned
Serial No.: Not yet assigned	
Filed: Herewith	
For: <i>Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same</i>	

**REQUEST TO USE COMPUTER READABLE FORM OF SEQUENCE LISTING
FROM PARENT APPLICATION PURSUANT TO 37 C.F.R. § 1.821 (e)**

Assistant Commissioner of Patents
Washington, D.C. 20231

Sir:

The patent application filed herewith is a continuing application of currently pending application Serial No. 09/866,028, filed on May 25, 2001. The Sequence Listings in (a) the herewith filed patent application and (2) currently pending patent application Serial No.09/866,028, filed on May 25, 2001, are identical. Therefore, pursuant to 37 C.F.R. § 1.821(e), Applicants respectfully request that the compliant computer readable form of the Sequence Listing filed on May 25, 2001 in parent application Serial No. 09/866,028 be used as the computer readable form for the herewith filed patent application. The paper copy of the Sequence Listing submitted herewith

09943780-083001

Serial No.: Not yet assigned
Filed: Herewith

is identical to that on the compliant computer readable form of the Sequence Listing filed on May 25, 2001 in parent application Serial No. 09/866,028.

Respectfully submitted,

GENENTECH, INC.

By: Elizabeth M. Barnes
Elizabeth M. Barnes, Ph.D.
Reg. No. 35,059
Telephone: (650) 225-4563



09157

PATENT TRADEMARK OFFICE

09943780-083001

Sequence Listing

<110> Baker, Kevin
 Botstein, David
 Eaton, Dan
 Ferrara, Napoleone
 Filvaroff, Ellen
 Gerritsen, Mary
 Goddard, Audrey
 Godowski, Paul
 Grimaldi, Christopher
 Gurney, Austin
 Hillan, Kenneth
 Kljavin, Ivar
 Napier, Mary
 Roy, Margaret
 Tumas, Daniel
 Wood, William

<120> SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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Pro Arg Ser His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro
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Gly Leu Thr Ser Val Pro Thr Asn Ile Pro Phe Asp Thr Arg Met
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Lys Leu Thr Lys Ile His Pro Lys Ala Phe Leu Thr Thr Lys Lys
140 145 150
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170 175 180
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185 190 195
Leu His Val Leu Glu Met Ser Ala Asn Pro Leu Asp Asn Asn Gly
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Asp Glu Thr Trp His Pro Asp Leu Gly Gln Pro Phe Gly Val Met
65 70 75

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Cys Cys Gln Thr Cys Pro Gln Glu Arg	Ser Ser Ser Glu Arg Gln	125	130	135
Pro Ser Gly Leu Ser Phe Glu Tyr Pro	Arg Asp Pro Glu His Arg	140	145	150
Ser Tyr Ser Asp Arg Gly Glu Pro Gly	Ala Glu Glu Arg Ala Arg	155	160	165
Gly Asp Gly His Thr Asp Phe Val Ala	Leu Leu Thr Gly Pro Arg	170	175	180
Ser Gln Ala Val Ala Arg Ala Arg Val	Ser Leu Leu Arg Ser Ser	185	190	195
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Val Pro Arg Leu Ser Leu Arg Leu Leu	Arg Ala Glu Gln Leu His	245	250	255
Val Ala Leu Val Thr Leu Thr His Pro	Ser Gly Glu Val Trp Gly	260	265	270
Pro Leu Ile Arg His Arg Ala Leu Ala	Ala Glu Thr Phe Ser Ala	275	280	285
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Arg Glu Leu Gln Ala Asn Val Ser Ala	Gln Glu Pro Gly Phe Ala	350	355	360
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380	385	390	
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Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser Glu Val	440	445	450
Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln Arg	455	460	465
Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr	470	475	480
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Pro Asp Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys	515	520	525
Gly His Ser Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly	530	535	540
Ala Leu Val Leu Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala	545	550	555
Trp Leu Ser Leu Asp Thr His Cys His Leu His Tyr Glu Val Leu	560	565	570
Leu Ala Gly Leu Gly Gly Ser Glu Gln Gly Thr Val Thr Ala His	575	580	585
Leu Leu Gly Pro Pro Gly Thr Pro Gly Pro Arg Arg Leu Leu Lys	590	595	600
Gly Phe Tyr Gly Ser Glu Ala Gln Gly Val Val Lys Asp Leu Glu	605	610	615
Pro Glu Leu Leu Arg His Leu Ala Lys Gly Met Ala Ser Leu Met	620	625	630
Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu Leu Arg Gly Gln Val	635	640	645
His Ile Ala Asn Gln Cys Glu Val Gly Gly Leu Arg Leu Glu Ala	650	655	660

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Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu Ala Pro	680	685	690
Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr Cys	695	700	705
Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro	710	715	720
Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr	725	730	735
Val Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His	740	745	750
Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys	755	760	765
Gln Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro	770	775	780
Gly Glu Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala	785	790	795
Gly Thr Arg Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys	800	805	810
Cys Ala Val Cys Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys	815	820	825
Glu Lys Val Gln Cys Pro Arg Leu Ala Cys Ala Gln Pro Val Arg	830	835	840
Val Asn Pro Thr Asp Cys Cys Lys Gln Cys Pro Val Gly Ser Gly	845	850	855
Ala His Pro Gln Leu Gly Asp Pro Met Gln Ala Asp Gly Pro Arg	860	865	870
Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro Glu Ser Gln Ser Trp	875	880	885
His Pro Ser Val Pro Pro Phe Gly Glu Met Ser Cys Ile Thr Cys	890	895	900
Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp Asp Cys Ser	905	910	915
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 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

<400> 12
 gtgctgccca tccgttctga gaagga 26

<210> 13

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
gcagggtgct caaacaggac ac 22

<210> 14
<211> 3231
<212> DNA
<213> Homo Sapien

<400> 14
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cttaactctg gtggtgaagg tcagcacctg tgtgccgggg gagagtcacg 1050

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tgaagaatac gatgcttgcc agaggaaacc ttgccaaaac aacgcgagct 1200
gtattgatgc aaatgaaaag caagatggga gcaatttcac ctgtgtttgc 1250
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 tcagtagtga gtattttctca tagtgcagct ttatttatct ccaggatgtt 3150
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 ccaaccatat tgaataaatg tgatcaagtc a 3231

<210> 15
 <211> 737
 <212> PRT
 <213> Homo Sapien

<400> 15
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 Ser Ser Leu Ala Asn Pro Val Pro Ala Ala Pro Leu Ser Ala Pro
 35 40 45
 Gly Pro Cys Ala Ala Gln Pro Cys Arg Asn Gly Gly Val Cys Thr
 50 55 60
 Ser Arg Pro Glu Pro Asp Pro Gln His Pro Ala Pro Ala Gly Glu
 65 70 75
 Pro Gly Tyr Ser Cys Thr Cys Pro Ala Gly Ile Ser Gly Ala Asn
 80 85 90
 Cys Gln Leu Val Ala Asp Pro Cys Ala Ser Asn Pro Cys His His
 95 100 105
 Gly Asn Cys Ser Ser Ser Ser Ser Ser Ser Asp Gly Tyr Leu

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110	115	120
Cys Ile Cys Asn Glu Gly Tyr Glu Gly	Pro Asn Cys Glu Gln Ala	
125	130	135
Leu Pro Ser Leu Pro Ala Thr Gly Trp	Thr Glu Ser Met Ala Pro	
140	145	150
Arg Gln Leu Gln Pro Val Pro Ala Thr	Gln Glu Pro Asp Lys Ile	
155	160	165
Leu Pro Arg Ser Gln Ala Thr Val Thr	Leu Pro Thr Trp Gln Pro	
170	175	180
Lys Thr Gly Gln Lys Val Val Glu Met	Lys Trp Asp Gln Val Glu	
185	190	195
Val Ile Pro Asp Ile Ala Cys Gly Asn	Ala Ser Ser Asn Ser Ser	
200	205	210
Ala Gly Gly Arg Leu Val Ser Phe Glu	Val Pro Gln Asn Thr Ser	
215	220	225
Val Lys Ile Arg Gln Asp Ala Thr Ala	Ser Leu Ile Leu Leu Trp	
230	235	240
Lys Val Thr Ala Thr Gly Phe Gln Gln	Cys Ser Leu Ile Asp Gly	
245	250	255
Arg Ser Val Thr Pro Leu Gln Ala Ser	Gly Gly Leu Val Leu Leu	
260	265	270
Glu Glu Met Leu Ala Leu Gly Asn Asn	His Phe Ile Gly Phe Val	
275	280	285
Asn Asp Ser Val Thr Lys Ser Ile Val	Ala Leu Arg Leu Thr Leu	
290	295	300
Val Val Lys Val Ser Thr Cys Val Pro	Gly Glu Ser His Ala Asn	
305	310	315
Asp Leu Glu Cys Ser Gly Lys Gly Lys	Cys Thr Thr Lys Pro Ser	
320	325	330
Glu Ala Thr Phe Ser Cys Thr Cys Glu	Glu Gln Tyr Val Gly Thr	
335	340	345
Phe Cys Glu Glu Tyr Asp Ala Cys Gln	Arg Lys Pro Cys Gln Asn	
350	355	360
Asn Ala Ser Cys Ile Asp Ala Asn Glu	Lys Gln Asp Gly Ser Asn	
365	370	375
Phe Thr Cys Val Cys Leu Pro Gly Tyr	Thr Gly Glu Leu Cys Gln	
380	385	390
Ser Lys Ile Asp Tyr Cys Ile Leu Asp	Pro Cys Arg Asn Gly Ala	
395	400	405

00000000000000000000000000000000

695

700

705

Ser Arg Pro Ala Met Tyr Asp Val Ser Pro Ile Ala Tyr Glu Asp
 710 715 720

Tyr Ser Pro Asp Asp Lys Pro Leu Val Thr Leu Ile Lys Thr Lys
 725 730 735

Asp Leu

<210> 16

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 16

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 17

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 18

<211> 508

<212> DNA

<213> Homo Sapien

<400> 18

ctctggaagg tcacggccac aggattccaa cagtgtctccc tcatagatgg 50

acgaaagtgt gacccccctt tcaggctttc aggggggactg gtctctctgg 100

aggagatgct cgccttgggg aataatcact ttattggttt tgtgaatgat 150

tctgtgacta agtctattgt ggctttgcgc ttaactctgg tggatgaagg 200

cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagggttcag 250

gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtgacc 300

tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350

gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400

aagatgggag caatttcacc tgtgtttgcc ttctgggta tactggagag 450

ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500

taggggag 508

<210> 19
<211> 508
<212> DNA
<213> Homo Sapien

<400> 19
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tctgtgacta agtctattgt ggctttgcgc ttaactctgg tgggaaggt 200
cagcacctgt gtgccggggg agagtcacgc aaatgacttg gagtggtcag 250
gaaaaggaaa atgcaccacg aagccgtcag aggcaacttt ttctgtacc 300
tgtgaggagc agtacgtggg tactttctgt gaagaatacg atgcttgcca 350
gaggaaacct tgccaaaaca acgcgagctg tattgatgca aatgaaaagc 400
aagatgggag caatttcacc tgtgtttgcc ttctgggta tactggagag 450
ctttgccaac cgaactgaga ttggagcgaa cgacctacac cgaactgaga 500
taggggag 508

<210> 20
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 20
ctctggaagg tcacggccac agg 23

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
ctcagttcgg ttggcaaagc tctc 24

<210> 22
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 22

cagtgtctccc tcatagatgg acgaaagtgt gacccccctt tcaggcgaga 50

gctttgccaa ccgaactga 69

<210> 23

<211> 1520

<212> DNA

<213> Homo Sapien

<400> 23

gctgagtctg ctgtctctgc tgctgtgtgt ccagcctgta acctgtgect 50

acaccacgcc agggcccccc agagccctca ccacgtggtg cgcccccaga 100

gcccacacca tgccgggcac ctacgtctcc tcgaccacac tcagtagtcc 150

cagcaccag ggctgcaag agcaggcacg ggccctgatg cgggacttcc 200

cgctcgtgga cggccacaac gacctgcccc tggctctaag gcagggtttac 250

cagaaagggc tacaggatgt taacctgcgc aatttcagct acggccagac 300

cagcctggac aggccttagag atggcctcgt gggcgcccag ttctggtcag 350

cctatgtgcc atgccagacc caggaccggg atgcctgcg cctcacctg 400

gagcagattg acctcatacg ccgcattgtg gctctctatt ctgagctgga 450

gcttgtgacc tcggctaaag ctctgaacga cactcagaaa ttggcctgcc 500

tcacgggtgt agaggggtggc cactcgtctg acaatagcct ctccatctta 550

cgtaccttct acatgtctggg agtgcgtctac ctgacgtca cccacacctg 600

caacacaccc tgggcagaga gctccgctaa gggcgctccac tccttctaca 650

acaacatcag cgggctgact gactttggtg agaaggtggt ggcagaaatg 700

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acggcgggcc ctggaagtgt cacaggcacc tgtgatcttc tcccactcgg 800

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Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala	185	190	195
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser	200	205	210
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val	215	220	225
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg	230	235	240
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly	245	250	255
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro	260	265	270
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys	275	280	285
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp	290	295	300
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr	305	310	315
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu	320	325	330
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg	335	340	345
Gln	Val	Glu	Lys	Val	Gln	Glu	Glu	Asn	Lys	Trp	Gln	Ser	Pro	Leu	350	355	360
Glu	Asp	Lys	Phe	Pro	Asp	Glu	Gln	Leu	Ser	Ser	Ser	Cys	His	Ser	365	370	375
Asp	Leu	Ser	Arg	Leu	Arg	Gln	Arg	Gln	Ser	Leu	Thr	Ser	Gly	Gln	380	385	390
Glu	Leu	Thr	Glu	Ile	Pro	Ile	His	Trp	Thr	Ala	Lys	Leu	Pro	Ala	395	400	405
Lys	Trp	Ser	Val	Ser	Glu	Ser	Ser	Pro	His	Met	Ala	Pro	Val	Leu	410	415	420
Ala	Val	Val	Ala	Thr	Phe	Pro	Val	Leu	Ile	Leu	Trp	Leu			425	430	

<210> 25

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25
agttctggtc agcctatgtg cc 22

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtgatggtg tctttgtcca tggg 24

<210> 27
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 27
ctccaccaat cccgatgaac ttgg 24

<210> 28
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 28
gagcagattg acctcatagc ccgcatgtgt gcctcctatt ctgagctgga 50

<210> 29
<211> 1416
<212> DNA
<213> Homo Sapien

<400> 29
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gatccgcggc cgcgaattct aaaccaacat gccgggcacc tacgctccct 100
cgaccacact cagtagtccc agcaccacagg gcctgcaaga gcaggcacgg 150
gccctgatgc gggacttccc gctcgtggac ggccacaacg acctgcccct 200
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atttcagcta cggccagacc agcctggaca ggcttagaga tggcctcgtg 300
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tgccctgcgc ctcacctgg agcagattga cctcatagc cgcattgtgtg 400

cctcctatct tgagctggag cttgtgacct cggctaaagc tctgaacgac 450
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 cagtctcaga gtcttcccc caccctgaca aaactcacac atgcccaccg 1350
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 aaaaccaag gacacc 1416

<210> 30
 <211> 446
 <212> PRT
 <213> Homo Sapien

<400> 30
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 Thr Gln Gly Leu Gln Glu Gln Ala Arg Ala Leu Met Arg Asp Phe
 20 25 30
 Pro Leu Val Asp Gly His Asn Asp Leu Pro Leu Val Leu Arg Gln
 35 40 45
 Val Tyr Gln Lys Gly Leu Gln Asp Val Asn Leu Arg Asn Phe Ser

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				65					70					75					
Ala	Gln	Phe	Trp	Ser	Ala	Tyr	Val	Pro	Cys	Gln	Thr	Gln	Asp	Arg					
				80					85					90					
Asp	Ala	Leu	Arg	Leu	Thr	Leu	Glu	Gln	Ile	Asp	Leu	Ile	Arg	Arg					
				95					100					105					
Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	Lys					
				110					115					120					
Ala	Leu	Asn	Asp	Thr	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	Glu					
				125					130					135					
Gly	Gly	His	Ser	Leu	Asp	Asn	Ser	Leu	Ser	Ile	Leu	Arg	Thr	Phe					
				140					145					150					
Tyr	Met	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	His	Thr	Cys	Asn					
				155					160					165					
Thr	Pro	Trp	Ala	Glu	Ser	Ser	Ala	Lys	Gly	Val	His	Ser	Phe	Tyr					
				170					175					180					
Asn	Asn	Ile	Ser	Gly	Leu	Thr	Asp	Phe	Gly	Glu	Lys	Val	Val	Ala					
				185					190					195					
Glu	Met	Asn	Arg	Leu	Gly	Met	Met	Val	Asp	Leu	Ser	His	Val	Ser					
				200					205					210					
Asp	Ala	Val	Ala	Arg	Arg	Ala	Leu	Glu	Val	Ser	Gln	Ala	Pro	Val					
				215					220					225					
Ile	Phe	Ser	His	Ser	Ala	Ala	Arg	Gly	Val	Cys	Asn	Ser	Ala	Arg					
				230					235					240					
Asn	Val	Pro	Asp	Asp	Ile	Leu	Gln	Leu	Leu	Lys	Lys	Asn	Gly	Gly					
				245					250					255					
Val	Val	Met	Val	Ser	Leu	Ser	Met	Gly	Val	Ile	Gln	Cys	Asn	Pro					
				260					265					270					
Ser	Ala	Asn	Val	Ser	Thr	Val	Ala	Asp	His	Phe	Asp	His	Ile	Lys					
				275					280					285					
Ala	Val	Ile	Gly	Ser	Lys	Phe	Ile	Gly	Ile	Gly	Gly	Asp	Tyr	Asp					
				290					295					300					
Gly	Ala	Gly	Lys	Phe	Pro	Gln	Gly	Leu	Glu	Asp	Val	Ser	Thr	Tyr					
				305					310					315					
Pro	Val	Leu	Ile	Glu	Glu	Leu	Leu	Ser	Arg	Gly	Trp	Ser	Glu	Glu					
				320					325					330					
Glu	Leu	Gln	Gly	Val	Leu	Arg	Gly	Asn	Leu	Leu	Arg	Val	Phe	Arg					
				335					340					345					

Gln Val Glu Lys	Val Gln Glu Glu Asn	Lys Trp Gln Ser Pro	Leu
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Glu Asp Lys Phe	Pro Asp Glu Gln Leu	Ser Ser Ser Cys His	Ser
365		370	375
Asp Leu Ser Arg	Leu Arg Gln Arg Gln	Ser Leu Thr Ser Gly	Gln
380		385	390
Glu Leu Thr Glu	Ile Pro Ile His Trp	Thr Ala Lys Leu Pro	Ala
395		400	405
Lys Trp Ser Val	Ser Glu Ser Ser Pro	His Pro Asp Lys Thr	His
410		415	420
Thr Cys Pro Pro	Cys Pro Ala Pro Glu	Leu Leu Gly Gly Pro	Ser
425		430	435
Val Phe Leu Phe	Pro Pro Lys Pro Lys	Asp Thr	
440		445	

<210> 31
 <211> 1790
 <212> DNA
 <213> Homo Sapien

<400> 31
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 cccggcagcg ccggccccat gcccgcgcgc cgccggggcc ccgcgcgcca 150
 atccgcgcgg cgggcgccgc cgttgcgtgc cctgcgtgctg ctgctctgcg 200
 tcctcggggc gccgcgagcc ggatcaggag ccacacacagc tgtgatcagt 250
 ccccaggatc ccacgcttct catcggtctc tccctgctgg ccacctgctc 300
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 tcaacggggc ccgcctgccc cctgagctct cccgtgtact caacgcctcc 400
 accttggtc tggccctggc caacctcaat ggggccaggc agcggtcggg 450
 ggacaacctc gtgtgccacg cccgtgacgg cagcatcctg gctggctcct 500
 gcctctatgt tggcctgccc ccagagaaac ccgtcaacat cagctgctgg 550
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 atggccagga caacacatgt gaggagtacc acacagtggg gcccactcc 700
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 ggaggccacc aaccgcctgg gctctgcccc ctccgatgta ctcacgctgg 800

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 tggttgagtt gcctagaacc cctgccaggg ctgggggtga gaaggggagt 1650
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 aaaaaaaaaa aaaaaaaaaa aaaaacaaaa aaaaaaaaaa 1790

<210> 32
 <211> 422
 <212> PRT
 <213> Homo Sapien

<400> 32
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 1 5 10 15
 Pro Pro Pro Leu Leu Pro Leu Leu Leu Leu Cys Val Leu Gly
 20 25 30
 Ala Pro Arg Ala Gly Ser Gly Ala His Thr Ala Val Ile Ser Pro
 35 40 45
 Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Leu Ala Thr Cys
 50 55 60

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Ser	Val	His	Gly	Asp	Pro	Pro	Gly	Ala	Thr	Ala	Glu	Gly	Leu	Tyr		65	70	75
Trp	Thr	Leu	Asn	Gly	Arg	Arg	Leu	Pro	Pro	Glu	Leu	Ser	Arg	Val		80	85	90
Leu	Asn	Ala	Ser	Thr	Leu	Ala	Leu	Ala	Leu	Ala	Asn	Leu	Asn	Gly		95	100	105
Ser	Arg	Gln	Arg	Ser	Gly	Asp	Asn	Leu	Val	Cys	His	Ala	Arg	Asp		110	115	120
Gly	Ser	Ile	Leu	Ala	Gly	Ser	Cys	Leu	Tyr	Val	Gly	Leu	Pro	Pro		125	130	135
Glu	Lys	Pro	Val	Asn	Ile	Ser	Cys	Trp	Ser	Lys	Asn	Met	Lys	Asp		140	145	150
Leu	Thr	Cys	Arg	Trp	Thr	Pro	Gly	Ala	His	Gly	Glu	Thr	Phe	Leu		155	160	165
His	Thr	Asn	Tyr	Ser	Leu	Lys	Tyr	Lys	Leu	Arg	Trp	Tyr	Gly	Gln		170	175	180
Asp	Asn	Thr	Cys	Glu	Glu	Tyr	His	Thr	Val	Gly	Pro	His	Ser	Cys		185	190	195
His	Ile	Pro	Lys	Asp	Leu	Ala	Leu	Phe	Thr	Pro	Tyr	Glu	Ile	Trp		200	205	210
Val	Glu	Ala	Thr	Asn	Arg	Leu	Gly	Ser	Ala	Arg	Ser	Asp	Val	Leu		215	220	225
Thr	Leu	Asp	Ile	Leu	Asp	Val	Val	Thr	Thr	Asp	Pro	Pro	Pro	Asp		230	235	240
Val	His	Val	Ser	Arg	Val	Gly	Gly	Leu	Glu	Asp	Gln	Leu	Ser	Val		245	250	255
Arg	Trp	Val	Ser	Pro	Pro	Ala	Leu	Lys	Asp	Phe	Leu	Phe	Gln	Ala		260	265	270
Lys	Tyr	Gln	Ile	Arg	Tyr	Arg	Val	Glu	Asp	Ser	Val	Asp	Trp	Lys		275	280	285
Val	Val	Asp	Asp	Val	Ser	Asn	Gln	Thr	Ser	Cys	Arg	Leu	Ala	Gly		290	295	300
Leu	Lys	Pro	Gly	Thr	Val	Tyr	Phe	Val	Gln	Val	Arg	Cys	Asn	Pro		305	310	315
Phe	Gly	Ile	Tyr	Gly	Ser	Lys	Lys	Ala	Gly	Ile	Trp	Ser	Glu	Trp		320	325	330
Ser	His	Pro	Thr	Ala	Ala	Ser	Thr	Pro	Arg	Ser	Glu	Arg	Pro	Gly		335	340	345
Pro	Gly	Gly	Gly	Ala	Cys	Glu	Pro	Arg	Gly	Gly	Glu	Pro	Ser	Ser				

350	355	360
Gly Pro Val Arg Arg Glu Leu Lys Gln	Phe Leu Gly Trp Leu Lys	
365	370	375
Lys His Ala Tyr Cys Ser Asn Leu Ser	Phe Arg Leu Tyr Asp Gln	
380	385	390
Trp Arg Ala Trp Met Gln Lys Ser His	Lys Thr Arg Asn Gln Asp	
395	400	405
Glu Gly Ile Leu Pro Ser Gly Arg Arg	Gly Thr Ala Arg Gly Pro	
410	415	420

Ala Arg

<210> 33
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 33
 cccgccccgac gtgcacgtga gcc 23

<210> 34
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
 tgagccagcc caggaactgc ttg 23

<210> 35
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 35
 caagtgcgct gcaaccctt tggcatctat ggctccaaga aagccgggat 50

<210> 36
 <211> 1771
 <212> DNA
 <213> Homo Sapien

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 ctccctagag tccttcgtga agctttttat tcctaagagg agaaaatcag 200
 tcaccggcga aatcgtgctg attacaggag ctgggcacatg aattgggaga 250
 ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
 tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg 350
 gtgccaaggt tcataccttt gtggtagact gcagcaaccg agaagatatt 400
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 aacattggaa aggatccttc ctgagcggtt cctggcagtt ttaaaacgaa 950
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 cccatttctt tcaatatcat ttttgaggct ttggcagctt tcatttacta 1150
 ccacttggtc tttagccaaa agctgattac atatgatata aacagagaaa 1200
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<210> 37
<211> 300
<212> PRT
<213> Homo Sapien

<400> 37

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Val	Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	20	25	30	
Arg	Lys	Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45	
His	Gly	Ile	Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	50	55	60	
Ser	Lys	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	65	70	75	
Thr	Ala	Ala	Lys	Cys	Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	80	85	90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	95	100	105	
Lys	Val	Lys	Ala	Glu	Ile	Gly	Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	110	115	120	
Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp	Leu	Phe	Ala	Thr	Gln	Asp	Pro	125	130	135	
Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn	Val	Leu	Ala	His	Phe	Trp	140	145	150	
Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr	Lys	Asn	Asn	His	Gly	155	160	165	
His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His	Val	Ser	Val	Pro	170	175	180	
Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	185	190	195	
His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile	Thr	Gly				

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200	205	210
Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly Phe		
215	220	225
Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu		
230	235	240
Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys		
245	250	255
Met Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu		
260	265	270
Arg Ile Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile		
275	280	285
Ser Val Lys Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln		
290	295	300

<210> 38

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 38

ggtgaaggca gaaattggag atg 23

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 39

atcccatgca tcagcctggt tacc 24

<210> 40

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

gctggtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 41

<211> 1377

<212> DNA

<213> Homo Sapien

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<400> 41

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aaaaaaaaa aaaaaaaaaa aaaaaaa 1377

<210> 42

<211> 243
 <212> PRT
 <213> Homo Sapien

<400> 42

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Ser	Pro	Pro	Leu	Asp	Asp	Asn	Lys	Ile	Pro	Ser	Leu	Cys	Pro	Gly	20	25	30	
His	Pro	Gly	Leu	Pro	Gly	Thr	Pro	Gly	His	His	Gly	Ser	Gln	Gly	35	40	45	
Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Ala	Pro	Gly	50	55	60	
Ala	Pro	Gly	Glu	Lys	Gly	Glu	Gly	Gly	Arg	Pro	Gly	Leu	Pro	Gly	65	70	75	
Pro	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Gly	Glu	Ala	Gly	Pro	Ala	Gly	80	85	90	
Pro	Thr	Gly	Pro	Ala	Gly	Glu	Cys	Ser	Val	Pro	Pro	Arg	Ser	Ala	95	100	105	
Phe	Ser	Ala	Lys	Arg	Ser	Glu	Ser	Arg	Val	Pro	Pro	Pro	Ser	Asp	110	115	120	
Ala	Pro	Leu	Pro	Phe	Asp	Arg	Val	Leu	Val	Asn	Glu	Gln	Gly	His	125	130	135	
Tyr	Asp	Ala	Val	Thr	Gly	Lys	Phe	Thr	Cys	Gln	Val	Pro	Gly	Val	140	145	150	
Tyr	Tyr	Phe	Ala	Val	His	Ala	Thr	Val	Tyr	Arg	Ala	Ser	Leu	Gln	155	160	165	
Phe	Asp	Leu	Val	Lys	Asn	Gly	Glu	Ser	Ile	Ala	Ser	Phe	Phe	Gln	170	175	180	
Phe	Phe	Gly	Gly	Trp	Pro	Lys	Pro	Ala	Ser	Leu	Ser	Gly	Gly	Ala	185	190	195	
Met	Val	Arg	Leu	Glu	Pro	Glu	Asp	Gln	Val	Trp	Val	Gln	Val	Gly	200	205	210	
Val	Gly	Asp	Tyr	Ile	Gly	Ile	Tyr	Ala	Ser	Ile	Lys	Thr	Asp	Ser	215	220	225	
Thr	Phe	Ser	Gly	Phe	Leu	Val	Tyr	Ser	Asp	Trp	His	Ser	Ser	Pro	230	235	240	
Val	Phe	Ala																

<210> 43
 <211> 24

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 43
 tacaggccca gtcaggacca gggg 24

 <210> 44
 <211> 18
 <212> DNA
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 <220>
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 <400> 44
 agccagcctc gctctcgg 18

 <210> 45
 <211> 18
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 45
 gtctgcgatc aggtctgg 18

 <210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 46
 gaaagaggca atggattcgc 20

 <210> 47
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 47
 gacttacact tgccagcaca gcac 24

 <210> 48
 <211> 45
 <212> DNA
 <213> Artificial Sequence

094337082460
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<220>

<223> Synthetic oligonucleotide probe

<400> 48

ggagcaccac caactggagg gtccggagta gcgagcgccc cgaag 45

<210> 49

<211> 1876

<212> DNA

<213> Homo Sapien

<400> 49

ctcttttgtc caccagccca gcctgactcc tggagattgt gaatagctcc 50

atccagcctg agaaacaagc cgggtggctg agccaggctg tgcacggagc 100

acctgacggg cccaacagac ccatgctgca tccagagacc tcccctggcc 150

gggggcatct cctggctgtg ctcttgcccc tcttggcac cacctgggca 200

gaggtgtggc caccacagct gcaggagcag gctccgatgg ccggagccct 250

gaacaggaag gagagtttct tgctcctctc cctgcacaac cgctgcgca 300

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cccgagcctg gcatccggcc tgtggcgcac cctgcaagtg ggctggaaca 450

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gcttcatggg gtcttcagag gcagacacct attacagagc caggatgaaa 1100

tgtcagagga aaggcggggg gctggccccag atcaagagcc agaaagtgc 1150

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Val Trp Leu Ser Ala Ala Met Gly Phe Gly Asn Cys Val Glu Leu
410 415 420

Gln Ala Ser Ala Ala Phe Asn Trp Asn Asp Gln Arg Cys Lys Thr
425 430 435

Arg Asn Arg Tyr Ile Cys Gln Phe Ala Gln Glu His Ile Ser Arg
440 445 450

Trp Gly Pro Gly Ser
455

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 51
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<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 52
gggtctgggc caggtggaag agag 24

<210> 53
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
gccaaggact ccttccgctg ggccacaggg gagcaccagg ccttc 45

<210> 54
<211> 2331
<212> DNA
<213> Homo Sapien

<400> 54
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 actccggcag accaaggatg cctcttcac aattctccat gacctccgac 1050
 cccaggaccg ttccagtatc attggatttt ccaaccggat caaagtatgg 1100
 aaggaccact tgatatcagt cactccagac agcatcaggg atgggaaagt 1150
 gtacattcac catatgtcac ccactggagg cacagacatc aacggggccc 1200
 tgcagagggc catcaggctc ctcaacaagt acgtggccca cagtggcatt 1250
 ggagaccgga gcgtgtccct catcgtcttc ctgacggatg ggaagcccac 1300
 ggtcggggag acgcacaccc tcaagatcct caacaacacc cgagaggccg 1350
 cccgaggcca agtctgcac ttaccattg gcacggcaa cgacgtggac 1400
 ttcaggctgc tggagaaact gtcgtggag aactgtggcc tcacacggcg 1450
 cgtgcacgag gaggaggacg caggctcgca gctcatcggg ttctacgatg 1500
 aaatcaggac cccgtcctc tctgacatcc gcacgatta tccccccagc 1550
 tcagtgggtgc aggccaccaa gacctgttc cccaactact tcaacggctc 1600
 ggagatcatc attgcgggga agctgggtgga caggaagctg gatcacctgc 1650

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Arg Val Lys Glu	Lys Arg Asn Lys Thr	Thr Glu Glu Asn Gly Glu	125	130	135
Lys Gly Thr Glu	Ile Phe Arg Ala Ser	Ala Val Ile Pro Ser Lys	140	145	150
Asp Lys Ala Ala	Phe Phe Leu Ser Tyr	Glu Glu Leu Leu Gln Arg	155	160	165
Arg Leu Gly Lys	Tyr Glu His Ser Ile	Ser Val Arg Pro Gln Gln	170	175	180
Leu Ser Gly Arg	Leu Ser Val Asp Val	Asn Ile Leu Glu Ser Ala	185	190	195
Gly Ile Ala Ser	Leu Glu Val Leu Pro	Leu His Asn Ser Arg Gln	200	205	210
Arg Gly Ser Gly	Arg Gly Glu Asp Asp	Ser Gly Pro Pro Pro Ser	215	220	225
Thr Val Ile Asn	Gln Asn Glu Thr Phe	Ala Asn Ile Ile Phe Lys	230	235	240
Pro Thr Val Val	Gln Gln Ala Arg Ile	Ala Gln Asn Gly Ile Leu	245	250	255
Gly Asp Phe Ile	Ile Arg Tyr Asp Val	Asn Arg Glu Gln Ser Ile	260	265	270
Gly Asp Ile Gln	Val Leu Asn Gly Tyr	Phe Val His Tyr Phe Ala	275	280	285
Pro Lys Asp Leu	Pro Pro Leu Pro Lys	Asn Val Val Phe Val Leu	290	295	300
Asp Ser Ser Ala	Ser Met Val Gly Thr	Lys Leu Arg Gln Thr Lys	305	310	315
Asp Ala Leu Phe	Thr Ile Leu His Asp	Leu Arg Pro Gln Asp Arg	320	325	330
Phe Ser Ile Ile	Gly Phe Ser Asn Arg	Ile Lys Val Trp Lys Asp	335	340	345
His Leu Ile Ser	Val Thr Pro Asp Ser	Ile Arg Asp Gly Lys Val	350	355	360
Tyr Ile His His	Met Ser Pro Thr Gly	Gly Thr Asp Ile Asn Gly	365	370	375
Ala Leu Gln Arg	Ala Ile Arg Leu Leu	Asn Lys Tyr Val Ala His	380	385	390
Ser Gly Ile Gly	Asp Arg Ser Val Ser	Leu Ile Val Phe Leu Thr	395	400	405
Asp Gly Lys Pro	Thr Val Gly Glu Thr	His Thr Leu Lys Ile Leu			

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410	415	420
Asn Asn Thr Arg Glu Ala Ala Arg Gly	Gln Val Cys Ile Phe Thr	
425	430	435
Ile Gly Ile Gly Asn Asp Val Asp Phe	Arg Leu Leu Glu Lys Leu	
440	445	450
Ser Leu Glu Asn Cys Gly Leu Thr Arg	Arg Val His Glu Glu Glu	
455	460	465
Asp Ala Gly Ser Gln Leu Ile Gly Phe	Tyr Asp Glu Ile Arg Thr	
470	475	480
Pro Leu Leu Ser Asp Ile Arg Ile Asp	Tyr Pro Pro Ser Ser Val	
485	490	495
Val Gln Ala Thr Lys Thr Leu Phe Pro	Asn Tyr Phe Asn Gly Ser	
500	505	510
Glu Ile Ile Ile Ala Gly Lys Leu Val	Asp Arg Lys Leu Asp His	
515	520	525
Leu His Val Glu Val Thr Ala Ser Asn	Ser Lys Lys Phe Ile Ile	
530	535	540
Leu Lys Thr Asp Val Pro Val Arg Pro	Gln Lys Ala Gly Lys Asp	
545	550	555
Val Thr Gly Ser Pro Arg Pro Gly Gly	Asp Gly Glu Gly Asp Thr	
560	565	570
Asn His Ile Glu Arg Leu Trp Ser Tyr	Leu Thr Thr Lys Glu Leu	
575	580	585
Leu Ser Ser Trp Leu Gln Ser Asp Asp	Glu Pro Glu Lys Glu Arg	
590	595	600
Leu Arg Gln Arg Ala Gln Ala Leu Ala	Val Ser Tyr Arg Phe Leu	
605	610	615
Thr Pro Phe Thr Ser Met Lys Leu Arg	Gly Pro Val Pro Arg Met	
620	625	630
Asp Gly Leu-Glu Glu Ala His Gly Met	Ser Ala Ala Met Gly Pro	
635	640	645
Glu Pro Val Val Gln Ser Val Arg Gly	Ala Gly Thr Gln Pro Gly	
650	655	660
Pro Leu Leu Lys Lys Pro Asn Ser Val	Lys Lys Lys Gln Asn Lys	
665	670	675
Thr Lys Lys Arg His Gly Arg Asp Gly	Val Phe Pro Leu His His	
680	685	690
Leu Gly Ile Arg		

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
gtgggaacca aactccggca gacc 24

<210> 57
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
cacatcgagc gtctctgg 18

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 58
agccgctcct tctccggttc atcg 24

<210> 59
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
tggaaggacc acttgatc agtcactcca gacagcatca gggatggg 48

<210> 60
<211> 1413
<212> DNA
<213> Homo Sapien

<400> 60
cggacgcgtg ggggtgcccga catggcgagt gtagtgctgc cgagcggatc 50
ccagtgtgcg gcggcagcgg cggcggcggc gcctcccggg ctccggcttc 100
tgctgttget cttctccgcc gcggcactga tccccacagg tgatgggcag 150
aatctgttta cgaaagacgt gacagtgatc gagggagagg ttgcgacat 200

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Ala	Ala	Ala	Ala	Ala	Pro	Pro	Gly	Leu	Arg	Leu	Leu	Leu	Leu	Leu	
				20					25						30
Phe	Ser	Ala	Ala	Ala	Leu	Ile	Pro	Thr	Gly	Asp	Gly	Gln	Asn	Leu	
				35					40						45
Phe	Thr	Lys	Asp	Val	Thr	Val	Ile	Glu	Gly	Glu	Val	Ala	Thr	Ile	
				50					55						60
Ser	Cys	Gln	Val	Asn	Lys	Ser	Asp	Asp	Ser	Val	Ile	Gln	Leu	Leu	
				65					70						75
Asn	Pro	Asn	Arg	Gln	Thr	Ile	Tyr	Phe	Arg	Asp	Phe	Arg	Pro	Leu	
				80					85						90
Lys	Asp	Ser	Arg	Phe	Gln	Leu	Leu	Asn	Phe	Ser	Ser	Ser	Glu	Leu	
				95					100						105
Lys	Val	Ser	Leu	Thr	Asn	Val	Ser	Ile	Ser	Asp	Glu	Gly	Arg	Tyr	
				110					115						120
Phe	Cys	Gln	Leu	Tyr	Thr	Asp	Pro	Pro	Gln	Glu	Ser	Tyr	Thr	Thr	
				125					130						135
Ile	Thr	Val	Leu	Val	Pro	Pro	Arg	Asn	Leu	Met	Ile	Asp	Ile	Gln	
				140					145						150
Lys	Asp	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ile	Glu	Val	Asn	Cys	Thr	
				155					160						165
Ala	Met	Ala	Ser	Lys	Pro	Ala	Thr	Thr	Ile	Arg	Trp	Phe	Lys	Gly	
				170					175						180
Asn	Thr	Glu	Leu	Lys	Gly	Lys	Ser	Glu	Val	Glu	Glu	Trp	Ser	Asp	
				185					190						195
Met	Tyr	Thr	Val	Thr	Ser	Gln	Leu	Met	Leu	Lys	Val	His	Lys	Glu	
				200					205						210
Asp	Asp	Gly	Val	Pro	Val	Ile	Cys	Gln	Val	Glu	His	Pro	Ala	Val	
				215					220						225
Thr	Gly	Asn	Leu	Gln	Thr	Gln	Arg	Tyr	Leu	Glu	Val	Gln	Tyr	Lys	
				230					235						240
Pro	Gln	Val	His	Ile	Gln	Met	Thr	Tyr	Pro	Leu	Gln	Gly	Leu	Thr	
				245					250						255
Arg	Glu	Gly	Asp	Ala	Leu	Glu	Leu	Thr	Cys	Glu	Ala	Ile	Gly	Lys	
				260					265						270
Pro	Gln	Pro	Val	Met	Val	Thr	Trp	Val	Arg	Val	Asp	Asp	Glu	Met	
				275					280						285
Pro	Gln	His	Ala	Val	Leu	Ser	Gly	Pro	Asn	Leu	Phe	Ile	Asn	Asn	
				290					295						300
Leu	Asn	Lys	Thr	Asp	Asn	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ser	Asn	

305	310	315
Ile Val Gly Lys Ala His Ser Asp Tyr	Met Leu Tyr Val Tyr Asp	
320	325	330
Pro Pro Thr Thr Ile Pro Pro Pro Thr	Thr Thr Thr Thr Thr Thr	
335	340	345
Thr Thr Thr Thr Thr Thr Ile Leu Thr	Ile Ile Thr Asp Ser Arg	
350	355	360
Ala Gly Glu Glu Gly Ser Ile Arg Ala	Val Asp His Ala Val Ile	
365	370	375
Gly Gly Val Val Ala Val Val Val Phe	Ala Met Leu Cys Leu Leu	
380	385	390
Ile Ile Leu Gly Arg Tyr Phe Ala Arg	His Lys Gly Thr Tyr Phe	
395	400	405
Thr His Glu Ala Lys Gly Ala Asp Asp	Ala Ala Asp Ala Asp Thr	
410	415	420
Ala Ile Ile Asn Ala Glu Gly Gly Gln	Asn Asn Ser Glu Glu Lys	
425	430	435
Lys Glu Tyr Phe Ile		
440		

<210> 62
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 62
 ggcttctgct gttgctcttc tccg 24

 <210> 63
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 63
 gtacactgtg accagtcagc 20

 <210> 64
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 64
atcatcacag attcccgagc 20

<210> 65
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
ttcaatctcc tcaccttcca ccgc 24

<210> 66
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
atagctgtgt ctgcgtctgc tgcg 24

<210> 67
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 67
cgcggcactg atccccacag gtgatgggca gaatctgttt acgaaagacg 50

<210> 68
<211> 2555
<212> DNA
<213> Homo Sapien

<400> 68
ggggcggtg gacgcggact cgaacgcagt tgcttcggga cccaggaccc 50
cctcggggcc gaccgcag gaaagactga ggccgcggcc tgccccggcc 100
ggctccctgc gccgcggcc cctcccggga cagaagatgt gctccagggt 150
ccctctgctg ctgccgtgc tctgtact ggccctgggg cctgggggtgc 200
agggtgccc atccggtgc cagtgcagcc agccacagac agtcttctgc 250
actgcccgcc aggggaccac ggtgccccga gacgtgccac ccgacacggt 300
ggggctgtac gtctttgaga acggcatcac catgctcgac gcaagcagct 350
ttgccggcct gccgggctg cagctcctgg acctgtcaca gaaccagatc 400

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110	115	120
Ala Leu Arg Leu	Ala Gly Leu Gly Leu	Gln Gln Leu Asp Glu Gly
125	130	135
Leu Phe Ser Arg	Leu Arg Asn Leu His	Asp Leu Asp Val Ser Asp
140	145	150
Asn Gln Leu Glu	Arg Val Pro Pro Val	Ile Arg Gly Leu Arg Gly
155	160	165
Leu Thr Arg Leu	Arg Leu Ala Gly Asn	Thr Arg Ile Ala Gln Leu
170	175	180
Arg Pro Glu Asp	Leu Ala Gly Leu Ala	Ala Leu Gln Glu Leu Asp
185	190	195
Val Ser Asn Leu	Ser Leu Gln Ala Leu	Pro Gly Asp Leu Ser Gly
200	205	210
Leu Phe Pro Arg	Leu Arg Leu Leu Ala	Ala Ala Arg Asn Pro Phe
215	220	225
Asn Cys Val Cys	Pro Leu Ser Trp Phe	Gly Pro Trp Val Arg Glu
230	235	240
Ser His Val Thr	Leu Ala Ser Pro Glu	Glu Thr Arg Cys His Phe
245	250	255
Pro Pro Lys Asn	Ala Gly Arg Leu Leu	Leu Glu Leu Asp Tyr Ala
260	265	270
Asp Phe Gly Cys	Pro Ala Thr Thr Thr	Thr Ala Thr Val Pro Thr
275	280	285
Thr Arg Pro Val	Val Arg Glu Pro Thr	Ala Leu Ser Ser Ser Leu
290	295	300
Ala Pro Thr Trp	Leu Ser Pro Thr Ala	Pro Ala Thr Glu Ala Pro
305	310	315
Ser Pro Pro Ser	Thr Ala Pro Pro Thr	Val Gly Pro Val Pro Gln
320	325	330
Pro Gln Asp Cys	Pro Pro Ser Thr Cys	Leu Asn Gly Gly Thr Cys
335	340	345
His Leu Gly Thr	Arg His His Leu Ala	Cys Leu Cys Pro Glu Gly
350	355	360
Phe Thr Gly Leu	Tyr Cys Glu Ser Gln	Met Gly Gln Gly Thr Arg
365	370	375
Pro Ser Pro Thr	Pro Val Thr Pro Arg	Pro Pro Arg Ser Leu Thr
380	385	390
Leu Gly Ile Glu	Pro Val Ser Pro Thr	Ser Leu Arg Val Gly Leu
395	400	405

Gln Arg Tyr Leu Gln Gly Ser Ser Val	Gln Leu Arg Ser Leu Arg
410	415 420
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr	
425	430 435
Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu	
440	445 450
Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro	
455	460 465
Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr	
470	475 480
Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg	
485	490 495
Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val	
500	505 510
Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg	
515	520 525
Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val	
530	535 540
Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro	
545	550 555
Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu	
560	565 570
Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met Gly Phe Pro Gly	
575	580 585
Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr Ile	
590	595

<210> 70
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 70
 ccctccactg cccaccgac tg 22

<210> 71
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 71
cggttctggg gacgttaggg ctcg 24

<210> 72
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 72
ctgcccaccg tccacctgcc tcaat 25

<210> 73
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aggactgccc accgtccacc tgcctcaatg ggggcacatg ccacc 45

<210> 74
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 74
acgcaaagcc ctacatctaa gccagagaga gacagggcag ctggg 45

<210> 75
<211> 1077
<212> DNA
<213> Homo Sapien

<400> 75
ggcactagga caaccttctt cccttctgca ccactgcccg tacccttacc 50
cgccccgcca cctccttgct accccactct tgaaaccaca gctgttgcca 100
gggtccccag ctcatgccag cctcatctcc tttcttgcta gcccccaaag 150
ggcctccagg caacatgggg ggcccagtc gagagccggc actctcagtt 200
gccctctggt tgagttgggg ggcagctctg ggggcccgtgg cttgtgccat 250
ggctctgctg acccaacaaa cagagctgca gagcctcagg agagaggtga 300
gccggctgca ggggacagga ggccccctccc agaatgggga agggatatccc 350
tggcagagtc tcccggagca gagttccgat gccctggaag cctgggagaa 400

tggggagaga tcccggaaaa ggagagcagt gctcacccaa aaacagaaga 450
 agcagcactc tgtcctgcac ctgggtccca ttaacgccac ctccaaggat 500
 gactccgatg tgacagaggt gatgtggcaa ccagctctta ggcgtgggag 550
 aggcctacag gccaaggat atggtgtccg aatccaggat gctggagttt 600
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 caggtggtgt ctcgagaagg ccaaggaagg caggagactc tattccgatg 700
 tataagaagt atgccctccc acccggaccg ggcctacaac agctgctata 750
 gcgcagggtg ctccattta caccaagggg atattctgag tgcataatt 800
 ccccgggcaa gggcgaaact taacctctct ccacatggaa ccttctctggg 850
 gtttgtgaaa ctgtgattgt gttataaaaa gtggctccca gcttggaaga 900
 ccaggggtggg tacatactgg agacagccaa gagctgagta tataaaggag 950
 agggaatgtg caggaacaga ggcattcttc tgggtttggc tcccgttcc 1000
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 cttgcttctg ttcccatgg agctccg 1077

<210> 76
 <211> 250
 <212> PRT
 <213> Homo Sapien

<400> 76
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro
 1 5 10 15
 Gly Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala
 20 25 30
 Leu Trp Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala
 35 40 45
 Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg
 50 55 60
 Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly
 65 70 75
 Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala
 80 85 90
 Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala
 95 100 105
 Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His Leu
 110 115 120

Val	Pro	Ile	Asn	Ala	Thr	Ser	Lys	Asp	Asp	Ser	Asp	Val	Thr	Glu
			125						130					135
Val	Met	Trp	Gln	Pro	Ala	Leu	Arg	Arg	Gly	Arg	Gly	Leu	Gln	Ala
			140						145					150
Gln	Gly	Tyr	Gly	Val	Arg	Ile	Gln	Asp	Ala	Gly	Val	Tyr	Leu	Leu
			155						160					165
Tyr	Ser	Gln	Val	Leu	Phe	Gln	Asp	Val	Thr	Phe	Thr	Met	Gly	Gln
			170						175					180
Val	Val	Ser	Arg	Glu	Gly	Gln	Gly	Arg	Gln	Glu	Thr	Leu	Phe	Arg
			185						190					195
Cys	Ile	Arg	Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser
			200						205					210
Cys	Tyr	Ser	Ala	Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu
			215						220					225
Ser	Val	Ile	Ile	Pro	Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro
			230						235					240
His	Gly	Thr	Phe	Leu	Gly	Phe	Val	Lys	Leu					
			245					250						

<210> 77
 <211> 2849
 <212> DNA
 <213> Homo Sapien

<400> 77
 cactttctcc ctctcttctt ttacttttcca gaaaccgcgc ttccgcttct 50
 ggctgcagag acctcggaga ccgcgccggg gagacggagg tgctgtgggt 100
 gggggggacc tgtggctgct cgtaccgccc cccaccctcc tcttctgcac 150
 tgccgtcttc cggaagacct tttcccttgc tctgttttct tcaccgagtc 200
 tgtgcatcgc cccggacctg gccgggagga ggcttggccg gcgggagatg 250
 ctctaggggc ggcgcgggag gagcggccgg cgggacggag ggcccggcag 300
 gaagatgggc tcccgtggac agggactctt gctggcgtag tgccctgctcc 350
 ttgcctttgc ctctggcctg gtcttgagtc gtgtgcccc tgtccagggg 400
 gaacagcagg agtgggaggg gactgaggag ctgccgtcgc ctccggacca 450
 tgccgagagg gctgaagaac aacatgaaaa atacaggccc agtcaggacc 500
 aggggctccc tgcttcccgg tgcttgcgct gctgtgaccc cggtaacctcc 550
 atgtaccgga cgaccgccgt gcccagatc aacatcacta tcttgaaagg 600
 ggagaagggt gaccgcggag atcgaggcct ccaagggaat tatggcaaaa 650

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caggctcagc agggggccagg ggccacactg gacccaaagg gcagaagggc 700
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 ggtggggccg aagaagccca tgcacagcaa ccactactac cagacggtga 800
 tcttcgacac ggagttcgtg aacctctacg accacttcaa catgttcacc 850
 ggcaagttct actgctacgt gcccggcctc tactttctca gcctcaacgt 900
 gcacacctgg aaccagaagg agacctacct gcacatcatg aagaacgagg 950
 aggaggtggt gatcttggtc ggcaggtgg ggcaccgag catcatgcaa 1000
 agccagagcc tgatgctgga gctgagagag caggaccagg tgtgggtacg 1050
 cctctacaag ggcgaacgtg agaacgccat cttcagcgag gagctggaca 1100
 cctacatcac cttcagtggc tacctggtca agcacgccac cgagccctag 1150
 ctggccggcc acctcctttc ctctcgccac cttccacccc tgcgctgtgc 1200
 tgacccacc gcctcttccc cgatccctgg actccgactc cctggctttg 1250
 gcattcagtg agacgccctg cacacacaga aagccaaagc gatcggtgct 1300
 cccagatccc gcagcctctg gagagagctg acggcagatg aaatcaccag 1350
 ggcggggcac ccgcgagaac cctctgggac cttccgcggc cctctctgca 1400
 cacatcctca agtgaccccc cagggcgaga cgcgggtggc ggcagggcgt 1450
 cccaggggtgc ggcaccgcgg ctccagtcct tggaaataat taggcaaatt 1500
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 ttttcagttg agactctgct taagagaaga tccaaagtta aagctctggg 1650
 gtcaggggag gggccggggg caggaaacta cctctggctt aattctttta 1700
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 ccagggaccc ctgggtcccc caggcctgca gatgtttcta tgaggggcag 1950
 agtccttgg tacatccatg tgtggctctg ctccaccct gtgccacccc 2000
 agagccctgg ggggtggtct ccatgcctgc caccctggca tcggctttct 2050
 gtgccgcctc ccacacaaat cagccccaga agggcccggg gccttggtt 2100

ctgtttttta taaaacacct caagcagcac tgcagtctcc catctcctcg 2150
 tgggctaagc atcaccgctt ccacgtgtgt tgtgttggtt ggcagcaagg 2200
 ctgatccaga ccccttctgc cccactgcc ctcatccagg cctctgacca 2250
 gtagcctgag aggggctttt tctaggcttc agagcagggg agagctggaa 2300
 ggggctagaa agctcccgtt tgtctgtttc tcaggctcct gtgagcctca 2350
 gtcttgagac cagagtcaag aggaagtaca cgtcccaatc acccgtgtca 2400
 ggattcactc tcaggagctg ggtggcagga gaggcaatag cccctgtggc 2450
 aattgcagga ccagctggag cagggttgcg gtgtctccac ggtgctctcg 2500
 cctgccccat ggccacccca gactctgata tccaggaacc ccatagcccc 2550
 tctccacctc acccatgtt gatgccagg gtcactcttg ctaccgctg 2600
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<212> PRT

<213> Homo Sapien

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 20 25 30

Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser
 35 40 45

Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr
 50 55 60

Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg
 65 70 75

Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro
 80 85 90

Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly
 95 100 105

Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly

110	115	120
Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly		
125	130	135
Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val		
140	145	150
Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val		
155	160	165
Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met		
170	175	180
Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe		
185	190	195
Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His		
200	205	210
Ile Met Lys Asn Glu Glu Glu Val Val Ile Leu Phe Ala Gln Val		
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln Ser Leu Met Leu Glu Leu		
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg Leu Tyr Lys Gly Glu Arg		
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp Thr Tyr Ile Thr Phe		
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
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0994380.033001

05943750-053001

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 tggttccaga taaaatcaac tgtttatata aatttctaata ggatttgctt 2200
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Lys Lys Ser Leu Glu	Asp Val Val Ile	Asp Ile Gln Ser Ser Leu	35	40	45
Ser Lys Gly Ile Arg	Gly Asn Glu Pro	Val Tyr Thr Ser Thr Gln	50	55	60
Glu Asp Cys Ile Asn	Ser Cys Cys Ser	Thr Lys Asn Ile Ser Gly	65	70	75
Asp Lys Ala Cys Asn	Leu Met Ile Phe	Asp Thr Arg Lys Thr Ala	80	85	90
Arg Gln Pro Asn Cys	Tyr Leu Phe Phe	Cys Pro Asn Glu Glu Ala	95	100	105
Cys Pro Leu Lys Pro	Ala Lys Gly Leu	Met Ser Tyr Arg Ile Ile	110	115	120
Thr Asp Phe Pro Ser	Leu Thr Arg Asn	Leu Pro Ser Gln Glu Leu	125	130	135
Pro Gln Glu Asp Ser	Leu Leu His Gly	Gln Phe Ser Gln Ala Val	140	145	150
Thr Pro Leu Ala His	His His Thr Asp	Tyr Ser Lys Pro Thr Asp	155	160	165
Ile Ser Trp Arg Asp	Thr Leu Ser Gln	Lys Phe Gly Ser Ser Asp	170	175	180
His Leu Glu Lys Leu	Phe Lys Met Asp	Glu Ala Ser Ala Gln Leu	185	190	195
Leu Ala Tyr Lys Glu	Lys Gly His Ser	Gln Ser Ser Gln Phe Ser	200	205	210
Ser Asp Gln Glu Ile	Ala His Leu Leu	Pro Glu Asn Val Ser Ala	215	220	225
Leu Pro Ala Thr Val	Ala Val Ala Ser	Pro His Thr Thr Ser Ala	230	235	240
Thr Pro Lys Pro Ala	Thr Leu Leu Pro	Thr Asn Ala Ser Val Thr	245	250	255
Pro Ser Gly Thr Ser	Gln Pro Gln Leu	Ala Thr Thr Ala Pro Pro	260	265	270
Val Thr Thr Val Thr	Ser Gln Pro Pro	Thr Thr Leu Ile Ser Thr	275	280	285
Val Phe Thr Arg Ala	Ala Ala Ala Thr	Leu Gln Ala Met Ala Thr Thr	290	295	300
Ala Val Leu Thr Thr	Thr Phe Gln Ala	Pro Thr Asp Ser Lys Gly			

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Ser Leu Glu Thr Ile Pro Phe Thr Glu	Ile Ser Asn Leu Thr Leu	
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Asn Thr Gly Asn Val Tyr Asn Pro Thr	Ala Leu Ser Met Ser Asn	
335	340	345
Val Glu Ser Ser Thr Met Asn Lys Thr	Ala Ser Trp Glu Gly Arg	
350	355	360
Glu Ala Ser Pro Gly Ser Ser Ser Gln	Gly Ser Val Pro Glu Asn	
365	370	375
Gln Tyr Gly Leu Pro Phe Glu Lys Trp	Leu Leu Ile Gly Ser Leu	
380	385	390
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395	400	405
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 <210> 86
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 <400> 86
 cgggtccctg ctctttgg 18

<210> 87
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<210> 90
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 cattccagat gcacccctgt ccagtgtgc ctatagcatc cgcagcatcg 150
 gggagaggcc tgtcctcaaa gctccagtc ccaaaaggca aaaatgtgac 200
 cactggactc cctgcccata tgacacctat gcttacaggt tactcagcgg 250
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 tgggagaaca gctgggaaat gttgccagag gaataaacat tgccattgtc 350
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 aatccctgct cttcatggtg acctatgacg acggaagcac aagactgaat 500

Asp	Ala	Lys	Asn	Ala	Ile	Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg
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Asn	Met	Lys	Phe	Arg	Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly
			185						190					195
Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser
			200						205					210
Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln
			215						220					225
Ile	Glu	Gly	Cys	Ile	Pro	Lys	Glu	Arg	Ser					
			230						235					

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<400> 94
 aagattcttg agcgattcca gctg 24

<210> 95
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ctcaagaagc acgcgtactg c 21

<210> 97
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catccaggct cgccactg 18

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<210> 105

<211> 21

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<213> Artificial Sequence

<220>

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<210> 106

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<223> Synthetic oligonucleotide probe

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<210> 108

<211> 19

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<400> 108

tggctcccag cttggaaga 19

<210> 109

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<210> 110

<211> 21

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<210> 113

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<210> 114

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide probe

<400> 116

ctatgaaatt aaccctcact aaagggacta ggggggtggga atgaaaag 48

<210> 117

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APPENDIX A

I hereby claim the benefit under Title 35, United States Code, §119(e) of any United States provisional applications listed below:

60/067,411 filed December 3, 1997;
60/069,334 filed December 11, 1997;
60/069,335 filed December 11, 1997;
60/069,278 filed December 11, 1997;
60/069,425 filed December 12, 1997;
60/069,696 filed December 16, 1997;
60/069,694 filed December 16, 1997;
60/069,702 filed December 16, 1997;
60/069,870 filed December 17, 1997;
60/069,873 filed December 17, 1997;
60/068,017 filed December 18, 1997;
60/070,440 filed January 5, 1998;
60/074,086 filed February 9, 1998;
60/074,092 filed February 9, 1998;
60/075,945 filed February 25, 1998;
60/112,850 filed December 16, 1998;
60/113,296 filed December 22, 1998;
60/146,222 filed July 28, 1999.

APPENDIX B

I hereby claim the benefit under Title 35, United States Code, §120 of any United States and PCT patent applications listed below:

PCT/US98/19330 filed September 16, 1998;

PCT/US98/25108 filed December 1, 1998;

09/216,021 filed December 16, 1998;

09/218,517 filed December 22, 1998;

09/254,311 filed March 3, 1999;

PCT/US99/12252 filed June 2, 1999;

PCT/US99/21090 filed September 15, 1999;

PCT/US99/28409 filed November 30, 1999;

PCT/US99/28313 filed November 30, 1999;

PCT/US99/28301 filed December 1, 1999;

PCT/US99/30095 filed December 16, 1999;

PCT/US00/03565 filed February 11, 2000;

PCT/US00/04414 filed February 22, 2000;

PCT/US00/05841 filed March 2, 2000;

PCT/US00/08439 filed March 30, 2000;

PCT/US00/14042 filed May 22, 2000;

PCT/US00/20710 filed July 28, 2000;

PCT/US00/32678 filed December 1, 2000;

PCT/US01/06520 filed February 28, 2001.